

F1: ASTLGSSTPKVDNAKKPFQPPREHVHVQVTH<sup>S</sup><sub>X</sub>MPPQKIEIFKSIEG<sup>W</sup><sub>R</sub>AEQNILV<sup>H</sup><sub>F</sub>LKPVEKWCWQ  
 F2: DFLPDP<sup>S</sup><sub>T</sub>EGFDEQVKELRARAKEIPDDYFVVVLVGDMITEEALPTYOTMLNTLLDGV  
 F3: DETGASLTPWAVWT  
 F4: DLLHTYLYLSGRV  
 F5: DMRQIQKTIQYLI  
 F6: TENSPYLGFIYTSFQER  
 F7: DV<sup>K</sup><sub>F</sub>LAQI<sup>C</sup><sub>Q</sub>GTIASDEKRRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKI<sup>S</sup><sub>T</sub>MPAHLMY  
 F8: DNLF  
 F9: dvFLAV<sup>A</sup><sub>I</sub>QRL<sup>G</sup><sub>I</sub>VYTAK  
 F10: DYADILEFLVGRWK  
 F11: VADLTGLSGEGRKA<sup>Q</sup><sub>G</sub>DYVCGLPPIRRIRLEERAQGRAKEGPVVPFSWIFDRQVKL

FIGURE 1

10

07/762762

# HindIII

1 GCTCACTTGTGTGGAGGAGAAAAACAGAACTCACAAAAAGCTTTGCGACTGCCAAGAACAACAACA 69  
42

70 ACAACAAGATCAAGAAGAAGAAGATCAAAAATGGCTCTTTCGAATCACTCCAGTGACCTTGCAA 138  
METAlaLeuArgIleThrProValThrLeuGln

## EcoRV

## BglII

## NcoI

139 TCGGAGAGATATCGTTTCGTTTCCTAAGAAGGCTAATCTCAGATCTCCCAAATTCGCCCATGGCC 207  
SerGluArgTyrArgSerPheSerPheProLysLysAlaAsnLeuArgSerProLysPheAlaMETAla  
149 185 201

## HindII

208 TCCACCCCTCGGATCATCCACACCGAAGGTTGACAAATGCCAAGAAGCCTTTTCAACCTCCACGAGAGGTT 276  
SerThrLeuGlySerSerThrProLysValAspAsnAlaLysLysProPheGlnProProArgGluVal  
238

277 CATGTTCAGGTGACGCCACTCCATGCCACCACAGAAAGATAGAGATTTTCAAATCCATCGAGGTTGGGCT 345  
HisValGlnValThrHisSerMETProProGlnLysIleGluIlePheLysSerIleGluGlyTrpAla

346 GAGCAGAACATATTGGTTCACCTAAAGCCAGTGGAGAAATGTTGGCAAGCACAGGATTTCCTGCCGGAC 414  
GluGlnAsnIleLeuValHisLeuLysProValGluLysCysTrpGlnAlaGlnAspPheLeuProAsp

FIGURE 2

Page 1 of 4

07/762762

415	CCTGCATCTGAAGGATTTGATGAACAAGTCAAGGAACCTAAGGGCAAGAGCAAAAGAGATTCTCTGATGAT	483
	ProAlaSerGluGlyPheAspGluGlnValLysGluLeuArgAlaArgAlaLysGluIleProAspAsp	
484	TACTTTGTTGTTGGTGGAGATATGATTACAGAGGAAGCCCTACCTACTTACCAAAACAATGCTTAAAT	552
	TyrPheValValLeuValGlyAspMETIleThrGluGluAlaLeuProThrTyrGlnThrMETLeuAsn	
553	ACCCTAGATGGTGTAACGTGATGAGACTGGGGCTAGCCCTTACGCCTTGGGCTGTCTGGACTAGGGCTTGG	621
	ThrLeuAspGlyValArgAspGluThrGlyAlaSerLeuThrProTrpAlaValTrpThrArgAlaTrp	
	PvuII	AccI
622	ACAGCTGAAGAGAACAGGCATGGCGATCTTCTCCACACCTATCTCTACCTTTCTGGCGGGTAGACATG	690
	ThrAlaGluGluAsnArgHisGlyAspLeuLeuHisThrTyrLeuTyrLeuSerGlyArgValAspMET	
	626	684
	BamHI	
691	AGGCAGATACAGAAGACAATTTCAGTATCTCATTTGGGTCAGGAATGGATCCTCGTACCGAAAAACAGCCCC	759
	ArgGlnIleGlnLysThrIleGlnTyrLeuIleGlySerGlyMETAspProArgThrGluAsnSerPro	
	736	
760	TACCTTGGGTTTCATCTACACATCGTTTCAAGAGCGTGCCACATTTGTTTCTACCGGAAACACCCGACAGG	828
	TyrLeuGlyPheIleTyrThrSerPheGlnGluArgAlaThrPheValSerHisGlyAsnThrAlaArg	

07/762762

SphI

|

829 CATGCAAGGATCATGGGACGTGAAACTGGCGCAAAATTTGTGTACAATCGCGTCTGACGAAAAGCGT 897  
HisAlaLysAspHisGlyAspValLysLeuAlaGlnIleCysGlyThrIleAlaSerAspGluLysArg  
833

Clai

|

898 CACGAGACCGCTTATACAAAGATAGTCGAAAAGCTATTTCGAGATCGATCCTGATGGCACCGTTCTTGCT 966  
HisGluThrAlaTyrThrLysIleValGluLysLeuPheGluIleAspProAspGlyThrValLeuAla  
942

BglII

|

967 TTTGCCGACATGATGAGGAAAAGATCTCGATGCCCGCACACTTGATGTACGATGGGCGTGATGACAAC 1035  
PheAlaAspMETMETArgLysLysIleSerMETProAlaHisLeuMETTyrAspGlyArgAspAspAsn  
990

AccI

|

1036 CTCTTCGAACATTTCTCGGCGGTTGCCCAAGACTCGGCGTCTACACCGCCAAAGACTACGCCGACATA 1104  
LeuPheGluHisPheSerAlaValAlaGlnArgLeuGlyValTyrThrAlaLysAspTyrAlaAspIle  
1077

1105 CTGGAATTTCTGGTCGGCGGTGGAAAGTGGCGGATTTGACCGGCCCTATCTGTGAAGGGCGTAAAGCG 1173  
LeuGluPheLeuValGlyArgTrpLysValAlaAspLeuThrGlyLeuSerGlyGlyArgLysAla

FIGURE 2

Page 3 of 4

07/762762

SacI

|

1174 CAAGATTATGTTTGGGGTTGCCACCAAGAATCAGAAGGCTGGAGGAGAGAGCTCAAGGGCGAGCAAAG 1242  
GlnAspTyrValCysGlyLeuProProArgIleArgArgLeuGluGluArgAlaGlnGlyArgAlaLys  
1228

PvuII

|

1243 GAAGGACCTGTTGTTCCATTTCAGCTGGATTTTCGATAGACAGGTGAAGCTGTGAAGAAAAAAACGA 1311  
GluGlyProValValProPheSerTrpIlePheAspArgGlnValLysLeu  
1266

1312 GCAGTGAGTTCGGGTTTCTGTGGCTTATTGGGTAGAGGTTAAACCTATTTTAGATGCTGTTCGTGT 1380

1381 AATGTGGTTTTTTTTTCTTAATCTGAATCTGGTATTGTGTCGTTGAGTTCGCGTGTGTGTAACCTTG 1449

1450 TGTGGCTGTGGACATATTATAGAAGCTCGTTATGCCAAATTTTGATGACGGTGGTTATCGTCTCCCCCTGGT 1518

1519 GTTTTTTTTATTGTTT 1533

1 AAAAGAAAAGGTAAGAAAAAACAATGGCTCTCAAGCTCAATCCTTTCTCCTTTCTCAAAACCCAAAAGT 69  
METAlaLeuLysLeuAsnProPheLeuSerGlnThrGlnLysL

BglII

|

70 TACCTTCTTTTCGCTCTTCCACCAATGGCCAGTACCAGATCTCCTAAGTTCTACATGGCCTCTACCCCTCA 138  
euProSerPheAlaLeuProProMETAlaSerThrArgSerProLysPheTyrMETAlaSerThrLeuL

139 AGTCTGGTTCTAAGGAAGTTGAGAAATCTCAAGAAGCCTTTTCATGCCCTCCGCGAGGTACATGTTTCAGG 207  
ysSerGlySerLysGluValGluAsnLeuLysLysProPheMETProProArgGluValHisValGlnV

208 TTACCCATTCTATTGCCA 225  
alThrHisSerIleAla

FIGURE 3A

AAAAGAAAAA GGTAAGAAAA AAAACA ATG GCT CTC AAG CTC AAT CCT TTC CTT TCT	56
MET Ala Leu Lys Leu Asn Pro Phe Leu Ser	
CAA ACC CAA AAG TTA CCT TCT TTC GCT CTT CCA CCA ATG GCC AGT ACC AGA TCT	110
Gln Thr Gln Lys Leu Pro Ser Phe Ala Leu Pro Pro MET Ala Ser Thr Arg Ser	
CCT AAG TTC TAC ATG GCC TCT ACC CTC AAG TCT GGT TCT AAG GAA GTT GAG AAT	164
Pro Lys Phe Tyr MET Ala Ser Thr Leu Lys Ser Gly Ser Lys Glu Val Glu Asn	
CTC AAG AAG CCT TTC ATG CCT CCT CGG GAG GTA CAT GTT CAG GTT ACC CAT TCT	218
Leu Lys Lys Pro Phe MET Pro Pro Arg Glu Val His Val Thr His Ser	
ATG CCA CCC CAA AAG ATT GAG ATC TTT AAA TCC CTA GAC AAT TGG GCT GAG GAG	272
MET Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Leu Asp Asn Trp Ala Glu Glu	
AAC ATT CTG GTT CAT CTG AAG CCA GTT GAG AAA TGT TGG CAA CCG CAG GAT TTT	326
Asn Ile Leu Val His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro Gln Asp Phe	
TTG CCA GAT CCC GCC TCT GAT GAT GGA TTT GAT GAG CAA GTC AGG GAA CTC AGG GAG	380
Leu Pro Asp Pro Ala Ser Asp Gly Phe Asp Glu Gln Val Arg Glu Leu Arg Glu	
AGA GCA AAG GAG ATT CCT GAT GAT TAT TTT GTT GTT TTG GGT GGA GAC ATG ATA	434
Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly Asp MET Ile	
ACG GAA GAA GCC CTT CCC ACT TAT CAA ACA ATG CTG AAT ACC TTG GAT GGA GTT	488
Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr MET Leu Asn Thr Leu Asp Gly Val	

07/762762

CGG GAT GAA ACA GGT GCA AGT CCT ACT TCT TGG GCA ATT TGG ACA AGG GCA TGG	542
Arg Asp Glu Thr Gly Ala Ser Pro Thr Ser Thr Trp Ala Ile Trp Thr Arg Ala Trp	
ACT GCG GAA GAG AAT AGA CAT GGT GAC CTC CTC AAT AAG TAT CTC TAC CTA TCT	596
Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Lys Tyr Leu Tyr Leu Ser	
GGA CGA GTG GAC ATG AGG CAA ATT GAG AAG ACA ATT CAA TAT TTG ATT GGT TCA	650
Gly Arg Val Asp MET Arg Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser	
GGA ATG GAT CCA CGG ACA GAA AAC AGT CCA TAC CTT GGG TTC ATC TAT ACA TCA	704
Gly MET Asp Pro Arg Thr Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser	
TTC CAG GAA AGG GCA ACC TTC ATT TCT CAT GGG AAC ACT GCC CGA CAA GCC AAA	758
Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg Gln Ala Lys	
GAG CAT GGA GAC ATA AAG TTG GCT CAA ATA TGT GGT ACA ATT GCT GCA GAT GAG	812
Glu His Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu	
AAG CGC CAT GAG ACA GCC TAC ACA AAG ATA GTG GAA AAA CTC TTT GAG ATT GAT	866
Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp	
CCT GAT GGA ACT GTT TTG GCT TTT GCT GAT ATG ATG AGA AAG AAA ATT TCT ATG	920
Pro Asp Gly Thr Val Leu Ala Phe Ala Asp MET MET Arg Lys Ile Ser MET	
CCT GCA CAC TTG ATG TAT GAT GGC CGA GAT GAT AAT CTT TTT GAC CAC TTT TCA	974
Pro Ala His Leu MET Tyr Asp Gly Arg Asp Asp Asn Leu Phe Asp His Phe Ser	



GCT GTT GCG CAG CAG CGT CTT GGA GTC TAC ACA GCA AAG GAT TAT GCA GAT ATA TTG	1028
Ala Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu	
GAG TTC TTG GTG GGC AGA TGG AAG GTG GAT AAA CTA ACG GGC CTT TCA GCT GAG	1082
Glu Phe Leu Val Gly Arg Trp Lys Val Asp Lys Leu Thr Gly Leu Ser Ala Glu	
GGA CAA AAG GCT CAG GAC TAT GTT TGT CGG TTA CCT CCA AGA ATT AGA AGG CTG	1136
Gly Gln Lys Ala Gln Asp Tyr Val Cys Arg Leu Pro Pro Arg Ile Arg Arg Leu	
GAA GAG AGA GCT CAA GGA AGG GCA AAG GAA GCA CCC ACC ATG CCT TTC AGC TGG	1190
Glu Glu Arg Ala Gln Gly Arg Ala Lys Glu Ala Pro Thr MET Pro Phe Ser Trp	
ATT TTC GAT AGG CAA GTG AAG CTG TAGGTGGCTA AAGTGCAGGA CGAAACCGAA ATGGTTAGTT	1254
Ile Phe Asp Arg Gln Val Lys Leu	
TCACTCTTTT TCATGCCCAT CCCTGCAGAA TCAGAAGTAG AGGTAGAATT TTGTAGTTGC TTTTTTATTA	1324
CAAGTCCAGT TTAGTTAAG GTCTGTGGAA GGGAGTTAGT TGAGGAGTGA ATTTAGTAAG TTGTAGATAC	1394
AGTTGTTTCT TGTGTTGTCA TGAGTATGCT GATAGAGAGC AGCTGTAGTT TTGTTGTTGT GTTCTTTTAT	1464
ATGGTCTCTT GTATGAGTTT CTTTTCTTTC CTTTTCTTCT TTCCCTTTCCCT CTCTCTCTCT CTCTCTCTCT	1534
CTCTTTTCT CTTATCCCAA GTGTCTCAAG TATAATAAGC AAACGATCCA TGTGGCAATT TTGATGATGG	1604
TGATCAGTCT CACAACCTGA TCCTTTGTCT TCTATTGGAA ACACAGCCTG CTTGTTTGAA AAAA	1668

FIGURE 3B

Page 3 of 3

07/762762

PCGN3235

1 TGAGAGATAGTGTGAGAGCATTAGCCTTAGAGAGAGAGAGAGAGCCTTGTGTCTGAAAGAATCCACAA 69

HindIII

70 ATGGCATTGAAGCTTAACCCCTTTGGCATCTCAGCCTTACAACCTTCCCT 117  
METAlaLeuLysLeuAsnProLeuAlaSerGlnProTyrAsnPhePro

FIGURE 4A

07/762762

PCGN3236

PstI

|

1 ACTTCATGGGCTATTGGACAAGAGCTTGGACTGCAGAAAGAGAACCCGACACGGTGATCTTCTCAATAAG 69  
ThrSerTrpAlaIleTrpThrArgAlaTrpThrAlaGluGluAsnArgHisGlyAspLeuLeuAsnLys

70 TATCTTTACTTGTCTGGACGTGTTGACATGAGGCAGATTGAAAAGACCATTCAGTACTTGATTGGTTCT 138  
TyrLeuTyrLeuSerGlyArgValAspMETArgGlnIleGluLysThrIleGlnTyrLeuIleGlySer

BamHI

|

139 GGAATGGATCCTAGAACAGAGAACAAATCCTTACCTCGG 176  
GlyMETAspProArgThrGluAsnAsnProTyrLeuAla

FIGURE 4B

07/762702

**PCGN3235**

TGAGAGATAG TGTGAGAGCA TTAGCCTTAG AGAGAGAGAG AGAGAGCTTG TGTCTGAAAG AATCCACAA

ATG GCA TTG AAG CTT AAC CCT TTG GCA TCT CAG CCT TAC AAC TTC CCT TCC TCG  
MET Ala Leu Lys Leu Asn Pro Leu Ala Ser Gln Pro Tyr Asn Phe Pro Ser Ser

GCT CGT CCG CCA ATC TCT ACT TTC AGA TCT CCC AAG TTC CTC TGC CTC GCT TCT  
Ala Arg Pro Pro Ile Ser Thr Phe Arg Ser Pro Lys Phe Leu Cys Leu Ala Ser

TCT TCT CCC GCT CTC AGC TCC AAG GAG GTT GAG AGT TTG AAG AAG CCA TTC ACA  
Ser Ser Pro Ala Leu Ser Ser Lys Glu Val Glu Ser Leu Lys Pro Phe Thr

CCA CCT AAG GAA GTG CAC GTT CAA GTC CTG CAT TCC ATG CCA CCC CAG AAG ATC  
Pro Pro Lys Glu Val His Val Gln Val Leu His Ser MET Pro Pro Gln Lys Ile

GAG ATC TTC AAA TCC ATG GAC TGG GCC GAG CAG AAC CTT CTA ACT CAG CTC  
Glu Ile Phe Lys Ser MET Glu Asp Trp Ala Glu Gln Asn Leu Thr Gln Leu

AAA GAC GTG AAG TCG TGG CAG CCC CAG GAC TTC TTA CCC GAC CCT GCA TCC  
Lys Asp Val Glu Lys Ser Trp Gln Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser

GAT GGG TTC GAA GAT CAG GTT AGA GAG CTA AGA GAG AGG GCA AGA GAG CTC CCT  
Asp Gly Phe Glu Asp Gln Val Arg Glu Leu Arg Ala Arg Glu Leu Pro

GAT GAT TAC TTC GTT GTT CTG GTG GGA GAC ATG ATC ACG GAA GAG GCG CTT CCG  
Asp Asp Tyr Phe Val Val Leu Val Gly Asp MET Ile Thr Glu Glu Ala Leu Pro

07/762762

ACC TAT CAA ACC ATG TTG AAC ACT TTG GAT GGA GTG AGG GAT GAA ACT GGC GCT  
Thr Tyr Gln Thr MET Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala

AGC CCC ACT TCA TGG GCT ATT TGG ACA AGA GCT TGG ACT GCA GAA GAG AAC CGA  
Ser Pro Thr Ser Trp Ala Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg

CAC GGT GAT CTT CTC AAT AAG TAT CTT TAC TTG TCT GGA CGT GTT GAC ATG AGG  
His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Tyr Ser Gly Arg Val Asp MET Arg

CAG ATT GAA AAG ACC ATT CAG TAC TTG ATT GGT TCT GGA ATG GAT CCT AGA ACA  
Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly MET Asp Pro Arg Thr

GAG AAC AAT CCT TAC CTC GGC TTC ATC TAC ACT TCA TTC CAA GAA AGA GCC ACC  
Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr

TTC ATC TCT CAC GGA AAC ACA GCT CGC CAA GCC AAA GAG CAC GGA GAC CTC AAG  
Phe Ile Ser His Gly Glu Asn Thr Ala Arg Gln Ala Lys Glu His Gly Asp Leu Lys

CTA GCC CAA ATC TGC GGC ACA ATA GCT GCA GAC GAG AAG CGT CAT GAG ACA GCT  
Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala

TAC ACC AAG ATA GTT GAG AAG CTC TTT GAG ATT GAT CCT GAT GGT ACT GTG ATG  
Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val MET

GCG TTT GCA GAC ATG ATG AGG AAG AAA ATC TCG ATG CCT GCT CAC TTG ATG TAC  
Ala Phe Ala Asp MET MET Arg Lys Lys Ile Ser MET Pro Ala His Leu MET Tyr

GAT GGG CGG GAT GAA AGC CTC TTT GAC AAC TTC TCT TCT TCT GTT GCT CAG AGG CTC  
 Asp Gly Arg Asp Glu Ser Leu Phe Asp Asn Phe Ser Ser Val Ala Gln Arg Leu  
 GGT GTT TAC ACT GCC AAA GAC TAT GCG GAC ATT CTT GAG TTT TTG GTT GGG AGG  
 Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Gly Arg  
 TGG AAG ATT GAG AGC TTG ACC GGG CTT TCA GGT GAA GGA AAC AAA GCG CAA GAG  
 Trp Lys Ile Glu Ser Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys Ala Gln Glu  
 TAC TTG TGT GGG TTG ACT CCA AGA ATC AGG AGG TTG GAT GAG AGA GCT CAA GCA  
 Tyr Leu Cys Gly Leu Thr Pro Arg Thr Pro Arg Ile Arg Arg Leu Asp Glu Arg Ala  
 AGA GCC AAG AAA GGA CCC AAG GTT CCT TTC AGC TGG ATA CAT GAC AGA GAA GTG  
 Arg Ala Lys Lys Gly Pro Lys Val Pro Phe Ser Trp Ile His Asp Arg Glu Val  
 CAG CTC TAA AAAGGAA CAAAGCTATG AAACCTTTTC ACTCTCCGTC GTCCCTCATT TGATCTATCT  
 Gln Leu \*  
 GCTCTTGAAA TTGGTGTAGA TTA CTATGGT TTGTGATATT GTTCGTGGGT CTAGTTACAA AGTTGAGAAG  
 CAGTGATTTA GTAGCTTTGT TGTTC CAGT CTTTAAATGT TTTTGTGTTT GGTCCTTTTA GTAAACTTGT  
 TGTAGTTAAA TCAGTTGAAC TGTTTGGTCT GT

07/762762

GAT	GCC	AAA	ANG	CCT	CAC	ATG	CCT	CCT	AGA	GAA	GCT	CAT	GTG	CAA	AAG	48
Asp	Ala	Lys	Xaa	Pro	His	MET	Pro	Pro	Arg	Glu	Ala	His	Val	Gln	Lys	
1				5					10					15		
ACC	CAT	TCA	ATK	CCG	CCT	CAA	AAG	ATT	GAG	ATT	TTC	AAA	TCC	TTG	GAG	96
Thr	His	Ser	Xaa	Pro	Pro	Gln	Lys	Ile	Glu	Ile	Phe	Lys	Ser	Leu	Glu	
				20				25					30			
GGT	TGG	GCT	GAG	GAG	AAT	GTC	TTG	GTG	CAT	CTT	AAA	CCT	GTG	GAG	AA	143
Gly	Trp	Ala	Glu	Glu	Asn	Val	Leu	Val	His	Leu	Lys	Pro	Val	Glu		
							40					45				

FIGURE 5

**Amino Acid  
Sequence From  
Fragment F2**

K	E	I	P	D	D	Y	FVVLVGD	MITEEALPTY	Q	T	M	L	N	T
AAA	GAA	AUU	CCN	GAU	GAU	UAU			CAA	ACN	AUG	CUN	AAU	AC/N
G	G	C		C	C	C			G					C

A

**Forward Primers:**

5'GCTAAGCTT	AAP	GAP	ATQ	CCA	GAQ	GAQ	TA3'	Desat 13-1
			A	CCG				Desat 13-2
				CCC				Desat 13-3
				CCT				Desat 13-4

**Reverse Primers:  
(complements)**

Desat 13-5a	3' GTQ TGN TAC GAN TTP TGCTTAAGCGA
Desat 13-6a	AAQ

**Oligonucleotides**

P = A or G  
Q = T or C  
N = A, C, T or C

FIGURE 6

07/762762



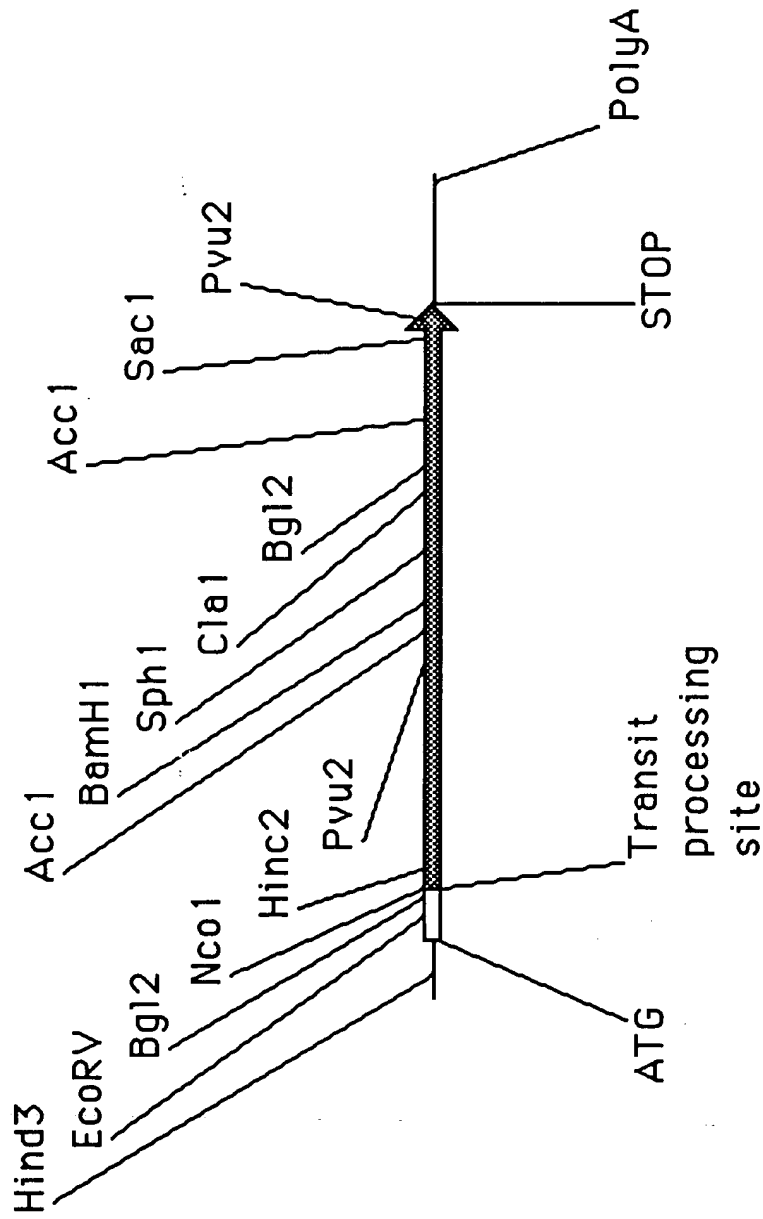


FIGURE 7A

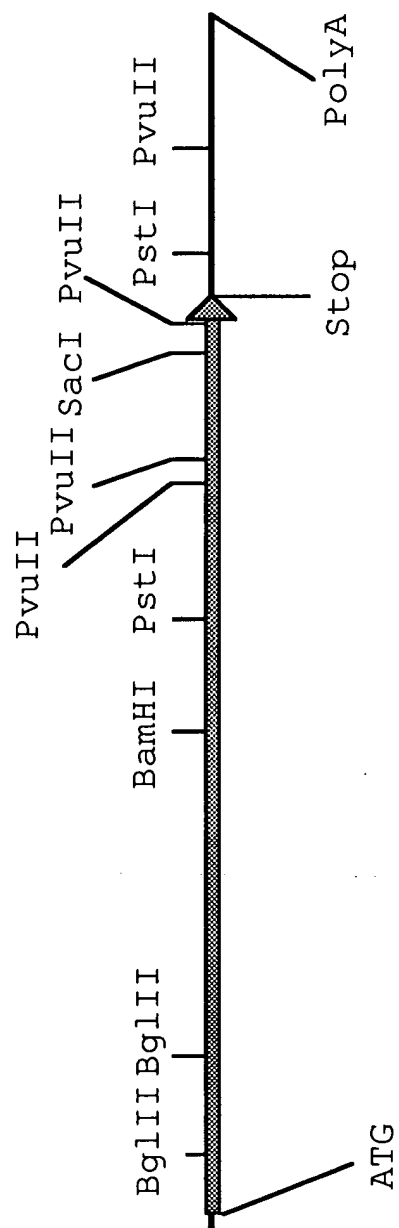


FIGURE 7B

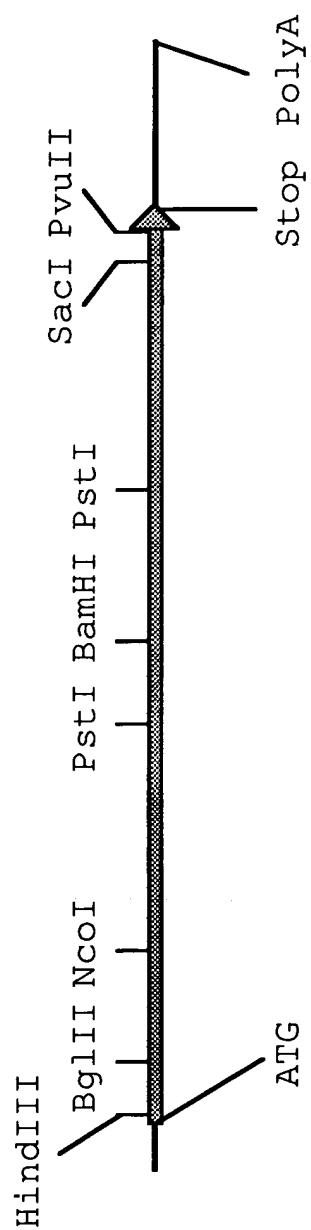


FIGURE 7C

TCTAGAAATC	TCTAATTACG	TCTGTTTGTT	CTATTTTTTA	TATGATATCA	AATATTCGTC	ATAAATATAT	70
GGTTTAAGAT	GCCAAAAAAT	TATTTACTTG	GTGAATATAA	TACGTTAAAT	ATTAGAAAATA	CATCATTTAG	140
TTAAATAAAT	AACCAAAAAC	CAAAAATTCA	TATCCGCGCT	GGCGGCGGGT	CAGGGTCTCG	TTAGTTTTAA	210
AATCAATGCA	GTTTACAATT	AATTTCCAGC	TGAAAATAAG	TATAATTGT	ATTGAAATTA	TAAAGTGACA	280
TTTTTTGTGT	AACAAATATT	TTGTGTAACA	AGAAATTAAAA	AAAAAAACAG	AAAATACTCA	GCTTTTTTAA	350
TAATAAAAAA	AATTAAATTGA	GTTAGAAAAAT	TGTTGTACCA	ATAACAAAAG	ATTTATATGG	AATTATAAAA	420
TCAACACACC	AATAACACAA	GACTTTTTTA	AAATTTAAGA	ATAATATAAG	CAATAACAAT	AGAATCTTCA	490
AATTCCTCAA	ATCCTTAAAA	ATCAATCTCC	CACTATTAAT	CCCCCTTAGT	TTTAGTTGGT	AATGGCAACG	560
TTTGTTGACT	ACCGTATTGT	AACTTTTGTC	AAATTGTCAT	AAATACGTGT	CAAACCTCTGG	TAAAAAATTA	630
GTCTGCTACA	TCTGTCTTTT	ATTTATAAAA	CACAGCTGTT	AATCAGAATT	TGGTTTATTA	AATCAACAAC	700
CTGCACGAAA	CTTGTGTGAG	CATATTTTGT	CTGTTTCTGG	TTCATGACCT	TCTTCCGCAT	GATGGCCAAAG	770
TGTAATGGCC	ACTTGCAAGA	GCGTTTCTTC	AACGAGATAA	GTCGAACAAA	TATTTGTCCG	TTACGACCAC	840
ATATAAAATC	TCCCCATCTC	TATATATAAT	ACCAGCATTC	ACCATCATGA	ATACCTCAA	TCCCAATCTC	910
ACAAATACTT	CAATAAAAAG	ACCAAAAAAA	ATTAAAGCAA	AGAAAAGCCT	TCTTGTGCAC	AAAAAATAAA	980

FIGURE 8  
Page 1 of 4

07/762762

GAAGCCTTCT AGGTTTTCAC GAC ATG AAG TTC ACT ACT CTA ATG GTC ATC ACA TTG	1036
MET Lys Phe Thr Thr Thr Leu MET Val Ile Thr Leu	
GTG ATA ATC GCC ATC TCG TCT CCT GTT CCA ATT AGA GCA ACC ACG GTT GAA AGT	1090
Val Ile Ile Ala Ile Ser Ser Pro Val Pro Ile Arg Ala Thr Thr Val Glu Ser	
TTC GGA GAA GTG GCA CAA TCG TGT GTT GTG ACA GAA CTC GCC CCA TGC TTA CCA	1144
Phe Gly Glu Val Ala Gln Ser Cys Val Val Thr Glu Leu Ala Pro Cys Leu Pro	
GCA ATG ACC ACG GCA GGA GAC CCG ACT ACA GAA TGC TGC GAC AAA CTG GTA GAG	1198
Ala MET Thr Thr Ala Gly Asp Pro Thr Thr Glu Cys Cys Asp Lys Leu Val Glu	
CAG AAA CCA TGT CTT TGT GGT TAT ATT CGA AAC CCA GCC TAT AGT ATG TAT GTT	1252
Gln Lys Pro Cys Leu Cys Gly Tyr Ile Arg Asn Pro Ala Tyr Ser MET Tyr Val	
ACT TCT CCA AAC GGT CGC AAA GTC TTA GAT TTT TGT AAG GTT CCT TTT CCT AGT	1306
Thr Ser Pro Asn Gly Arg Lys Val Leu Asp Phe Cys Lys Val Pro Phe Pro Ser	
TGT TAAATCTCTC AAGACATTGC TAAGAAAAAT ATTATTAAAA ATAAAAGAAT CAAACTAGAT	1369
Cys	
CTGATGTAAC AATGAATCAT CATGTTATGG TTGAAGCTTA TATGCTGAAG TGTTTGATTT TATATATGTG	1439
TGTGTGTGTG TCCTGCTCAA TTTTGTGAAAC ACACACGTTT CTCCTGATTT GGATTTAAAT TATATTTTGA	1509
GTAAAAAAA AGAAAAAGAT GGAATGCTAT TTATACAAAGT TGATGAAAAA GTGGAAGTAC AATTAGATA	1579

TCCTCTACAC	TTAAAGAATG	AAACAATAAT	AGACTTACGA	AACAAATGAA	AAATACATAA	ATTGTCGACA	1649
ATCAACGTCC	GATGACGAGT	TTATTATTAA	AAATTGTGT	GAAGGACTAG	CAGTTCAACC	AAATGATATT	1719
GAACATATAC	ATCAACAAAT	ATGATAATCA	TAAAAGAGAG	AATGGGGGGG	GGGTGTCGTT	TACCAGAAAC	1789
CTCTTTTCT	CAGCTCGCTA	AAACCCCTACC	ACTAGAGACC	TAGCTCTGAC	CGTCGGCTCA	TCGGTGCCGG	1859
AGGTGTAACC	TTTCTTTCCC	ATGACCCGAA	ACCTCTCTTT	CCCAACTCAC	GAAAACCCCTA	CAATCAAAAA	1929
CCTAGCTCCG	ACCGTCGGCT	CATCGGTGCC	GAAGGTGTAA	CCTTTCTCTC	CCATCATAGT	TTCTCGTAAA	1999
TGAAAGCTAA	TTGGGCAATC	GATTTTTTAA	TGTTTAAACC	ATGCCAAGCC	ATTTCTTATA	GGACAAATTGT	2069
CAATAATAGC	ATCTTTTGAG	TTTTGTCTCA	AAAGTGACAC	TAGAAGAAAA	AAGTCACAAA	AATGACATTTC	2139
ATTAAAAAGT	AAAATATCCC	TAATACCTTT	GGTTTAAATT	AAATAAGTAA	ACAAAAATAA	ATAAAAACAA	2209
ATAAAATAAA	AATAAAAAAT	GAAAAAAAGA	AATTTTTTAA	TAGTTTCAGA	TTATATGTTT	TCAGATTTCGA	2279
AATTTTTTAA	ATCCCTTTT	TTAAATTTTC	TTTTTTGAAA	TTTTTTTTTT	TGAAATTTTT	TGAAACTGTT	2349
TTTAAAAATT	TTATTTTTAA	TTTTTTTAGTA	TTTATTTTTT	ATTTTATAAA	ATTTTAAACG	CTAATTCCAA	2419
AACTCCCCCC	CCCCCCCCCC	CCCCAATTCT	CTCCTAGTCT	TTTTCTCTTT	CTTATATTG	GGCTTCTATC	2489
TTCTCTTTTT	TTTTCAGGCC	CAAAGTATCA	TGTGTAACAA	CCGGTGTTCA	AAAACGCGCC	CGCCTGGCCG	2559

FIGURE 8  
Page 3 of 4

07/762762

TTTACTCGCC	CGATTAAATG	ATGATCGGAA	GGCTGCCATG	GCGAGGCGGA	GGTAATCAGT	GGTTCTAGGC	2629
GCTGAAACTA	GAAAACCTTC	AAAAATCGAA	ATTTTAAGAG	CTAAATCGGT	GTTTATCTCA	TGAATCTATT	2699
ATATTTAGTT	GAAACTCACA	AGAAATCGGTT	GTAATAACTA	TGAAATCGTG	CAAAAAAAAT	GAAGAACAAA	2769
ATATTCTCAG	ATCTGGAAAA	CACAGAGAAG	AGGTTGAAGA	TGAGGGTAAA	ATCGTATTTT	GTCATTCTTT	2839
AAACTAAAT	CAAAAAAAA	TGATGCAAAA	TTCAATGATA	ATAACTCGAA	CTCGCAACCA	TATGCATCTT	2909
TAGACTGCGA	CACGGACCAC	TAGACTAAGC	AATTTTAATG	TTTATTCAATC	ACAGACCCTAA	TATAATGTCTA	2979
AAACTAGGCG	CCGAGTACGC	CCCGCTTAAT	CCCGAGTTT	TGTTAGCTCG	CTAGACCCAG	GGTCACCGCC	3049
CGACTAACGA	GTAGCGTAAT	TCTGAACTGG	GGTAACAACA	TAGAGAACAT	CGCCGACCCCT	TCCCTGCCGA	3119
TGATGCCGCC	TCCGATGAAC	TTCCTGTAAAC	GCCTTCAGTT	TCCATTGATT	TTCCCCCTTTA	ATCTGATCAG	3189
TTCCATGTTT	TATCCAACTC	ATCCCACTCC	GTAGCATTTA	ATCGATCTCA	TCATTTACAT	ACATAAACCCAG	3259
TAGGAGGTCT	CATATAAATT	TGAACGTTTC	CAGCGATGAA	CAGTGCCCAAT	CTCTGCGAAA	TCCATTTCTC	3329
TAAGCTCAGG	GCTGGCGGCT	GCAGCCCGGG	GATCCACTAG	TTCTAGGCGG	CCGCACCGCG	GTGGAGCTCC	3399
AATTCGCCCT	ATAGTGAGTC	GTATTACGCG	CGCTCACTGG	C			3440

XhoI

1

1 CTCGAGAGCTGAAGGATTTTGTAGAGATTCAACGACAGATGGACCCCTTCCTCCACTAGGCAACTGC 69

2

70 AAGAACCTAACAAATGCAAATATCACTCCTCCTCAGCCCTTCAAGGAGCGTTAATAGGACTGGAACAAGCG 138

BglII

1

139 GTCAAGTGAGTAAATTTTCCTTCCAAGATAGATCTCTATGGTTCGGTTCATGAAGTTTGTGGTTAATT 207

169

208 GTGTAGCAACAGGATAGTGCAAGTGAGAATAGAGTTCGACCTCATCTACCTACCCCGGAACCTCTGAAT 276

277 GTATCCCCATTGAAGAAGAAGAGGGCAAATCCTGCACCCAGAAAGGATAAAGAAATTTTGGACGCCCTGAA 345

346 GAAGTGGCAGTTCTGAGGGAAGGAGTAAAAGAGTATGTCTACTACTACTCTATAATCAAGTTTCAA 414

415 GAAGCTGAGCTTGGCTCTCACTTTATATGTTTGTGTTGTGCAGGTATGTAATCATGGAAAAGAG 483

484 ATAAAGAAATGCAAAACCCTGAAGTATTGGCAGAGAGGACTGAGGTGAGAGAGCATGTCACTTTTGTGTTA 552

553 CTCATCTGAATTATCTTATATGCGAATTGTAAGTGGTACTAAAAGGTTTGTAACTTTTGGTAGGTGGAT 621

622 TTGAAGGATAAATGGAGGAACCTTGCTTCGGTAGCGGTAACAAGTTTATATTGCTATGAAGTTTTTTTG 690

691 CCTGCGTGACGTATCAGCAGCTGTGGAGAAGATGGTATTAGAAAGGGTCTTTTCACATTTTGTGTTGTG 759

FIGURE 9

Page 1 of 6

07/762762



760 ACAAATATTAATTCGGCCGGTATGGTTTGGTTAAGACTTGTGAGAGACGTGTGGGGTTTTTTGATGTA 828  
829 TAATTAGTCTGTGTTTAGAACGAAACAAGACTTGTGCGTATGCTTTTTTAACTTGAGGGGGTTTGT 897  
BglII  
|  
898 GTTGTAGTTAGGAACCTTGACTTTGTCTCTTTCTCTCAAGATCTGATTGGTAAGGTCTGGGTGGTAGTA 966  
937  
967 CTGTTTGGTTTAAATTTTGGACTATTGAGTCACTGTGGCCCCATTGACTTTTAAATTAGGCTGGTATAT 1035  
1036 TTTTGGTTTAAACCGGCTGAGATAGTGCAATTTTCGATTCAGTCAATTTTAAATTCTTCAAGGTAAT 1104  
1105 GGGCTGAATACTTGTATAGTTTTTAAGACTTAAACAGGCCCTTAAAGGCCCATGTTATCATATAAACGTCAT 1173  
HindIII  
|  
1174 TGTTAGAGTGCACCAAGCTTATAAAATGTAGCCAGGCCCTTAAAGACTTAAACAGGCCCTTAAAGACTT 1242  
1190  
1243 AACATTCCTTAAAGGCCCATGTTATCATATAAACGTCAATCGTTTTGAGTGCACCAAGCTAAATGTAGCC 1311  
1312 AGGCCTTAAAGACTTAAACAGGCCCTTAAAGGCCCATGTTATCATATAAACGCCGCGTTTTGAGTGCAC 1380

# HindIII

1381 CAAGCTTATAAATGTAGCCAGCTACCTCGGGACATCACGCTCTTTGTACACTCCGCCATCTCTCTCTCT 1449  
1383

## XhoI BglII

## SalI

1450 CTCGAGCAGATCTCTCTCGGGAATATCGACAATGTGACCACTTTCTGCTCTTCCGCTCTCCATGCAAGC 1518  
1451 1458 1484

1519 CACTTCTCTGTAATCTCATCTCCTTCTTGTTGCCAGATCGCTCTGATCATACTTTCTTTAGATCA 1587

1588 TTTGCCCTCTGATCTGTTGCTTGATGTTTAACTCTCCACGCATGTTTGATTATGTTGAGAAATTAGAA 1656

1657 AAAAAATGTTAGCTTTACGAATCTTTAGTGATCATTTCAATTGGATTGCAATCTTGTGTGACATTGA 1725

1726 GGCTTGTGTAGATTTCGATCTGTATTCAATTTGAATCACAGCTATAAATAGTCATTTGAGTAGTAGTGT 1794

1795 TTAAATGAACATGTTTGTGTTGATGGAACAAAACAGGCAGCAACACGAGGATTAGTTTCCAGAA 1863

1864 GCCAGCTTTGGTTTCAACGACTAATCTCTCCTTCAACCTCCGCCGTTCAATCCCCACTCGTTTCTCAAT 1932

1933 CTCCTGCGCGGTAATGTTCTCATTTCTCAGCATTTAATTTTCGAGCTTGCTTGTCAATGGTACTCTCTCTAAT 2001

2002 GTCTATTTGGTTTATTAGGCCAAACCAGAGACGGTTGAGAAAGTGTCTAAGATAGTTAAGAGCAGCTA 2070

FIGURE 9

Page 3 of 6

07/762762

2071 TCACTCAAAGACGACCAAAAGGTCGTTGCCGGAGACCAAGTTTGCTGATCTTGGAGCAGATTCTCTCGAC 2139  
2140 ACTGTAAGTCATCAATCATCTCTTATGTGAATAAAGAGAACTTGAAGAGTTTGTGTTTAAACATATTAA 2208

EcoRV

2209 CTGAGTGTTTTGCGATGCAGGTTGAGATAGTGATGGGTTTAGAGGAAGAGTTTGATATCGAAAATGGCTGA 2277  
2264

SstI

2278 AGAGAAAAGCTCAGAAAGATTGCTACTGTGGAGGAAGCTGCTGAACTCATTTGAAGAGCTCGTTCAACTTAA 2346  
2335

2347 GAAGTAATTTTAGTATTAAGAGCAGCCAAGGCTTTGTTGGGTTTGTGTTTTCATAAATCTTCCGTGCAT 2415  
2416 TTTCTTTTCTTTAATGTGTCAAGCGACTCTGTTGGTTTAAAGTAGTATCTGTTGCCATGGATCTCTC 2484

SalI

HindIII

2485 TCTATTTGTCGACTGAAAACCTTTTGGTTTACACATGAAAGCTTGTTCCTTGTCTTTCTTAAATCGAAAT 2553  
2493 2523

2554 GCCAAATGCGAGATTAGGGAATCTTGTATTAAACACATACATAAAGTCAAAGAGTAGGCCCTAAGATGACA 2622  
2623 ATTTATAACAATCCTATTTCACATTGTATATACAGGTTATGATTATCCCAATCAGCGTCAAAGAATCC 2691

2692 AGCATCTTTCATCTCTGAAATAGTAGACATTCTCCAAGTTCACATCTTCTCCTGCACCAAAAACCAGTA 2760  
2761 CTAAATCATGAACATTGCAATAATCACATGCCCTAGGCGAGAGTTTTGGTGATGTGGTGTAGTGATAGT 2829  
2830 GATACTGATGGTGCTAGAGCGGTTAAGAAGGATTAACTGGAAAGTCTGCAAGGAAAGTAACATAGA 2898  
2899 GAAGAGGAAGATAGGAGTGGTAACAAACACTTGTGATCCCCATACAGCCTCCCAGCATTTTTCAAAATGTT 2967  
2968 ATTTCCCTTACATAAAGAAAACAAGAGAAGTCTGACTAGATGATATTTATATAGGATAAGTGTTTACCAT 3036  
3037 AAGCCAAAGTGAGCGCCGTTTGCAAGAGCTAACCCAGACAGTACACGTTTGGCATAATATCTCATCAACAT 3105  
3106 GATCTGAAAAGTAACATATCACAGTTAATGAACACAAATGGTTACCTTGAGAAAGCAAATCAAGACCCTATA 3174  
3175 ACAAGCCCAGAGATGAGGAAAGTCCGTGTCAACGCTTCACCGCCATTTCGCGTAGTTTCCTTGGAAAGACA 3243  
3244 AAGGCCACCAACCAACTTACTTCCAGAAACAACACTCCAAATGTTGTCAACAAGTCAATAGATTCCA 3312  
3313 AACTACTTCGTTACAGGGTTGTATAGATAATAATAAGTAGTGGGAAGATAGTATAAAATAAAATAAA 3381  
3382 TAAAAGATCCTATCGGTAAATAGTTTATAATATCGGGGCGTATATAAAGTATAAAAGAAACTCTTCTC 3450  
3451 CAATCCGACCGTTGAAAATCACTCTCAATCTCTGGCGTAACGACCGGATCGTTCGCGGTAATTTTCGC 3519  
3520 TGCTATAAATAGAAACTTTCCCTCTTCTGTTTCTCGATCAAAAATTTTTTTTGGAAAAATTAAAGTTTGAA 3588

3589 TCTATCGTAGATGCTGTGACAAAAAATTGTTTATCGAAGATGAGAAACATGAGGCCCTGTTTCATGC 3657

BamHI

|

3658 AAGGAACCAGACCCACGGATCCATCTTCGCCGATGATGACGTCTCCTCTGATGAATCGTCACGCACGGAC 3726  
3674

BamHI

|

3727 AGGATCCAAACGCTGGACCAGCATCTAACGCCAAGAAAGCACAGACGAAAGCAGCTCAGAGACTCGC 3795  
3729

3796 GGCTGTGATGTCGAACCAACAGGCGACGATGAAGACAGTGATGACCTTTCCTTTGACTACAACGC 3864

BglII

|

3865 TGTCGGAAGCATTGGTCTCGCTGCCCGGAAGATCT 3898  
3894

07/762762

Lambda CGN1-2

NCG-186 Linear

LENGTH = 4325

```

      XhoI      SduI      NlaIV      HgiJII      HindIII
      |         |         |         |         |
1  CTCGAGGCAGTCACTAACATGAAGTTTGACGAGGAGCCCCAACTATGGGAAGCTTATTCTCTTTTCGAT 69
2
      36
      XbaI      SacI
      |         |
70 ACTCTAATTGAGCCGTGCGCTCTATCTAGACCAATTAGAAATTGATGGAGCTCTAAAGTTGCTGGCTGT 138
95
      NdeI      SspI      NdeI
      |         |         |
139 TTTCTTGTTCATATGATTAACTTCTAAACTTGTGTATAAATATTCTCTGAAAGTGCTTCTTTTGGCATA 207
150
      180
      Ksp632I
      |
208 TGTAGGTTGGGCAAAAACGAGGAAGATTGCTTCTCAATTTGGAAGAGGATGAACAGCCGAAGAAGAAAA 276
245
```

FIGURE 10

Page 1 of 13

07/762762

XhoI

|

277 TAAGAAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATAACGGTCGTCGTCCCATGAACAGAGGT 345  
305

MmeI EcoRV

|

346 AAAACATTTTTGCGATATACACTTTGAAAGTTCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA 414  
401 408

SduI

MstI

BclI HgiAI

|

|

415 CAATGTCGGAGAGACAA3GGCTGMNCAATATACAAAAGGAAATGAAGATGGCCCTTTTGTAGTAGCTG 483  
437 442  
439

HaeI

|

469

SduI

HgiJII

|

484 TGTAGCATCAGCAGCTAATCTCTGGGCTCTCATCATGATGCTGGAACTGGATTCACTTCTCAAGTTA 552  
512

FIGURE 10  
Page 2 of 13

07/762762

Cfr10I

BbvII

| |

553 TGAGTTGTCACCCGGTCTTCCTACACAAGGTAATAATCAGTTGAAGCAATTAAGAATCAATTGATTGT 621  
560

563

622 AGTAAACTAAGAAGAACTTACCTTATGTTTCCCGCAGGACTGGATTATGGAACAAATGGGAAAAGAAC 690

SacI

|

691 TACTATATAAGCTCCATAGCTGGTTCAGATAACGGGAGCTCTTTAGTTGTTATGTCAAAAGGTTAGTGT 759  
731

BbvII

|

760 TTAGTGAATAATAAACTTATACCCACAAAAGTCTTTCATTGACTTATTTATATACTTGTGTAATTGCTAG 828  
782

829 GAACTACTTATTCTCAGCAGTCATACAAAAGTGAGTGACTCATTTCCGTTCAAGTGGATAAAATAAGAAAT 897

898 GAAAGAAGATTTTCATGTAACTCCATGACAACTGCTGGTAATCGTTGGGGTGTGGTAATGTCGAGGA 966

BclI

|

967 ACTCTGGCTTCTCTGATCAGGTAGGTTTTTGTCTCTTATTGTCTGGTGTTTTATTTTCCCTGATAGT 1035  
981



1036 CTAATATGATAAACTCTGCGTTGTGAAAGGTGGTGGAGCTTGACTTTTGTACCCCAAGCGATGGGATAC 1104  
 1105 ATAGGAGTGGGAGAATGGGTATAGAATAACATCAATGGCAGCAACTGCGGATCAAGCAGCTTTCATAT 1173  
     Tth1111111  
         |  
 1174 TAAGCATACCAAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCACCACCGCCTTTCCAAAGTA 1242  
     1175  
                     ScaI  
                         |  
 1243 CTCATGTCAAGGTGGTTTCTTTAGCTTTGAACACAGATTTGGATCTTTTGTGTTTGTTCATATACT 1311  
                     XhoII  
                         |  
                     1285  
 1312 TAGGACCTGAGAGCTTTTGGTTGATTTTTTTTCAGGACAAATGGGCGAAGAATCTGTACATTGCATCA 1380  
                     AflIII  
                         |  
 1381 ATATGCTATGGCAGGACAGTGTGCTGATACACACTTAAAGCATCATGTGGAAAGCCAAAGACAAATTGGAG 1449  
                     1415  
 1450 CGAGACTCAGGGTCGTCATAATACCAATCAAAGACGTAAACCAGACGCAACCTCTTTGGTTGAATGTA 1518  
                     SspI  
                         |  
 1519 ATGAAAGGGATGTGCTTGGTATGTATGTACGAATAACAAAGAGAAGATGGAATTAGTAGTAAATA 1587  
                     1587

FIGURE 10  
 Page 4 of 13

07/762762

1588	TTTGGGAGCTTTTAAAGCCCTTCAAGTGIGCTTTTATCTTATTGATATCATCCATTGCGTTGTTAA	1656	EcoRV 
		1635	
			XbaI 
1657	TGCGTCTCTAGATATGTTCCCTATATCTTTCTCAGTGTCTGATAAGTGAAATGTGAGAAAACCATACCAA	1725	
		1664	
			SspI 
1726	ACCAAAATATTCAAATCTTATTTTAAATAATGTTGAATCACTCGGAGTTGCCACCTTCTGTGCCAATTG	1794	
		1734	
			EcoRI 
1795	TGCTGAATCTATCACACTAGAAAAAACATTTCTCAAGGTAATGACTTGTGGACTATGTTCTGAATTC	1863	
		1859	
			Eco57I 
1864	TCATTAAAGTTTTTATTTTCTGAAGTTTAAAGTTTTTACCTTCTGTGTTTGAATAATATCGTTCATAAGATG	1932	
		1904	

SphI  
 NspI  
 |  
 1933 TCACGCCAGGACATGAGCTACACATCGCACATAGCATGCAGATCAGGACGATTTGTCACTCACTTCAAA 2001  
 1971  
  
 Tth111111  
 |  
 2002 CACCTAAGAGCTTCTCTCACAGCGCACACACATATGCATGCAATATTACACGATCGCCATGCAA 2070  
 2015  
 2037 2048 2053  
 2036 2044 2056  
  
 NdeI SphI NspI PmaCI  
 [AvaIII] SspI AflIII  
 || | | |  
 2071 ATCTCCATTCTCACCTATAAATTAGAGCCTCGGCTTCACTCTTTACTCAAAACCAAACTCATCACTACA 2139  
 2099  
  
 Ksp632I  
 |  
 2140 GAACATACACAAATGGCGAACAAGCTCTTCCTCGTCTCGGCAACTCTCGCCTTGTTCCTTCTCACC 2208  
 METAlaAsnLysLeuPheLeuValSerAlaThrLeuAlaLeuPheLeuLeuThr  
 2171

SecI  
 |  
 2099





AccI

|

2830 TACTCCGTAGACGGTAATAAAGAGAGAAGTTTTTTTTTACTCTTGCTACTTTTCCATATAAAGTGATGAT 2898  
2838

SpeI  
ScaI

| |

VspI

|

2899 TAACAACAGATACACCCAAAAGAAAACAATTAACTATATTCAACAATGAAGCAGTACTAGTCTATTGAA 2967  
2929  
2954  
2955

NspI

AflIII

| |

2968 CATGTCAGATTTTCTTTTCTAAATGTCTAATTAAAGCCTTCAAGGCTAGTGATGATAAAGATCATCCA 3036  
2968  
2972

XhoII

NlaIV

BamHI

| |

MmeI

BclI

|

3037 ATGGGATCCCAACAAGACTCAAAATCTGGTTTTTGATCAGATACTTCAAAACTATTTTGTATTCATTAA 3105  
3041  
3043

07/762762

	BbvII		Tth111
3106	TTATGCAAGTGTCTTTTATTGGTGAAGACTCTTTAGAAAGCAAGAACGACAGTAATAAAAAA		3174
	3139		3174
		VspI	
3175	ACAAAGTTCAGTTTAAAGATTGTTATTGACTTATTGTCAATTTGAAAAATATAGTATGATATTAAATATA		3243
			3237
		VspI	
3244	GTTTTATTATATAAATGCTTGCTATTCAAGATTGAGAACATTAATATGATACTGTCCACATATCCAA		3312
3250			3287
	NdeI	Tth111	
3313	TATATTAAGTTTCATTCTGTTCAAACATATGATAAGATGGTCAAAATGATTATGAGTTTGTATTAC		3381
	3341	3352	
	Eco57I		
3382	CTGAAGAAAAGATAAGTGAGCTTCGAGTTTCTGAAGGGTACGTGATCTTCATTTCTTGGCTAAAAGCGA		3450
	3404	3434	
		Eco57I	
3451	ATATGACATCACCTAGAGAAAGCCGATAATAGTAACTCTGTTCTTGGTTTTTGGTTTAATCAAACCGA		3519





EcoRV

|

3865 CCTTTGGTGGATATCGTGACGAAGGACCTCCCAGTGAAGTCATTGGTTCGTTTACTCTTTTCTTAG 3933  
3880

HindIII

AflII

|

3934 TCGAATCTTATTCTTGCTCTGCTCGTTGTTTTTACCGATAAAGCTTAAAGACTTTATTGATAAAGTTCTCA 4002  
3977  
3974

4003 GCTTTGAATGTGAATGAACGTGTTTCCTGCTTATTAGTGTTCCCTTTGTTTGAAGTTGAATCACTGCTTA 4071

4072 GCACTTTTGTAGATTCACTTTTGTGTTTAAAGTTAAAGGTAGAAACTTTGTGACTTGTCTCCGTTATG 4140

HpaI

HindII

|

4141 ACAAGGTTAACTTTGTTGGTTATAACAGAAAGTTGCGACCTTTCTCCATGCTTGTGAGGGTGATGCTGTG 4209  
4149

Tth111II

|

4179

XhoII

|

4210 GACCAAGCTCTCTCAGGCGGAAGATCCCTTACTTCAATGCCCCCAATCTACTTGGAAAAACAAGACACAGAT 4278  
4231

07/762762

07/762762

FIGURE 10